

GenCore version 5.1.6
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Om protein - protein search, using bw model

Run on: February 17, 2005, 15:19:48 ; Search time 0.001 Seconds

(without alignments)
 258.063 Million cell updates/sec

Title: us-10-036-342-57

Perfect score: 2623

Sequence: 1 MDPKLGGRMMAASLLAVILLL.....NYIETKLIFFAFLPLEMAQLH 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1 seqs, 509 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : aay76144.geneseqp2000b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	2612.5	99.6	509	1 AAY76144 Human secreted pro

ALIGNMENTS

RESULT 1

AAY76144

ID AAY76144 Standard; Protein; 509 AA.

XX AC AAY76144;

XX DT 23-MAR-2000 (first entry)

XX DB Human secreted protein encoded by gene 21.

XX Human; secreted protein; cancer; tumour; developmental abnormality;

XX foetal deficiency; blood disorder; immune system disorder; inflammation;

XX autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;

XX schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;

XX atherosclerosis; diabetes; cardiovascular disorder; kidney disorders,

XX digestive/endocrine disorders; infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown

CC in AAY76224 to AAY76424 represent fragments of the secreted proteins

CC XX SQ Sequence 509 AA:

Query Match Similarity 99.6%; Score 2612.5; DB 1; Length 509;

Matches 507; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDPKLGGRMMAASLLAVILLLRLERGMFSSPPPPALSKVFOYDHLDEFEVTLKENVIA 59

Db 1 MDPKLGGRMMAASLLAVILLLRLERGMFSSPPPPALSKVFOYDHLDEFEVTLKENVIA 59

QY 60 ESDSVQPVPERFRGLERFMRMVAADTQLQIGARVASVDMGQQLPDGOSLPPVIAELG 119

Db 61 ESDSVQPVPERFRGLERFMRMVAADTQLQIGARVASVDMGQQLPDGOSLPPVIAELG 120

QY 120 SDPPIKGTVCFYGLDVAQDRDGWLTDPYVTEVDGKLYGAGATNGKPYLAWINAVSA 179

Db 121 SDPPIKGTVCFYGLDVAQDRDGWLTDPYVTEVDGKLYGAGATNGKPYLAWINAVSA 180

QY 180 FRALEQDLPVNPKITRGMERAGSVALEELVEKEKORFFPSGVYDVTISDNLWISORKPA 239

Db 181 FRALEQDLPVNPKIFIGMEAGSVALEELVEKEKORFFPSGVYDVTISDNLWISORKPA 240

XX PD 18-NOV-1999.

XX PR 06-MAY-1999; 99W0-US009847.

XX PR 12-MAY-1998; 98US-0085093P.

PR 12-MAY-1998; 98US-0085105P.

PR 12-MAY-1998; 98US-0085180P.

PR 18-MAY-1998; 98US-0085960P.

PR 18-MAY-1998; 98US-0085900P.

PR 18-MAY-1998; 98US-0085921P.

PR 18-MAY-1998; 98US-0085922P.

PR 18-MAY-1998; 98US-0085933P.

PR 18-MAY-1998; 98US-0085924P.

PR 18-MAY-1998; 98US-0085925P.

PR 18-MAY-1998; 98US-0085927P.

PR 18-MAY-1998; 98US-0085928P.

OY 300 VPLTEEBINTYKAHLDEBEYRNSRVEKFLEPTKEELMHLWRYPSLINCIGARDEP 359
Db 301 VPLTEEBINTYKAHLDEBEYRNSRVEKFLEPTKEELMHLWRYPSLINCIGARDEP 360
OY 360 GTKWVIGRVIGKESIRLYPHMNSAVEKQVTHLEDVFSKRNUSSNQVSMVLGHWTI 419
Db 361 GTKWVIGRVIGKESIRLYPHMNSAVEKQVTHLEDVFSKRNUSSNQVSMVLGHWTI 420
OY 420 ANIDDTQMLAKGAIARTWFGTEPMIRDGSTIPAKMFOETIARKSVVTLPLGAVIDGEHS 479
Db 421 ANIDDTQMLAKGAIARTWFGTEPMIRDGSTIPAKMFOETIARKSVVTLPLGAVIDGEHS 480
OY 480 QNEKINRWNVIEGTKLPAFFLEMQH 507
Db 481 QNEKINRWNVIEGTKLPAFFLEMQH 508

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